#6

Page: 1

Raw Sequence Listing

10/23/91 11:12:04

1 2		SEQUENCE LISTING
3		
<u>4</u> 5	(1) GENE	RAL INFORMATION:
6	(i)	APPLICANT: CAPUT, DANIEL
7		FERRARA, PASCUAL
8		GUILLEMOT, JEAN-CLAUDE
9		KAGHAD, MOURAD
10		LEGOUX, RICHARD
11		LOISON, GERARD
12		LARBRE, ELIZABETH
13		LUPKER, JOHANNES
14		LEPLATOIS, PASCUAL
15		SALOME, MARK
16		
17	(ii)	TITLE OF INVENTION: URATE OXIDASE ACTIVITY PROTEIN,
18		RECOMBINANT GENE CODING THEREFOR, EXPRESSION VECTOR
19		MICRO-ORGANISMS AND TRANSFORMED CELLS
20		
21	(iii)	NUMBER OF SEQUENCES: 35
22		
23	, ,	CORRESPONDENCE ADDRESS:
24	• 1	(A) ADDRESSEE: Foley & Lardner
25		(B) STREET: 1800 Diagonal Road, Suite 500
26		(C) CITY: Alexandria
27		(D) STATE: Virginia
28		(E) COUNTRY: USA
29		(F) ZIP: 22313-0299
30	4>	
31 32	(▼)	COMPUTER READABLE FORM:
		(A) MEDIUM TYPE: Floppy disk
33 34		(B) COMPUTER: IBM PC compatible
35		(C) OPERATING SYSTEM: PC-DOS/MS-DOS
36		(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
37	(mi)	CURDELIN ADDITIONAL DAMA.
38	(41)	CURRENT APPLICATION DATA:
39		(A) APPLICATION NUMBER: US 07/659,408
40		(B) FILING DATE: 25-APR-1991
41		(C) CLASSIFICATION:
42	/:::\	ATTORNEY/AGENT INFORMATION:
43	(VIII)	(A) NAME: BENT, Stephen A.
44		• •
45		(B) REGISTRATION NUMBER: 29,768 (C) REFERENCE/DOCKET NUMBER: 16781/276 BEDL
46		(C) REFERENCE/DUCKET NUMBER: 16/81/2/6 BEDL
47	/iv\	TELECOMMUNICATION INFORMATION:
48	(14)	(A) TELEPHONE: (703)836-9300
49		(B) TELEFAX: (703)683-4109
50		(C) TELEX: 899149
51		(V) ADDIA: UJJIEJ
52		
53	(2) TNFO	RMATION FOR SEQ ID NO:1:
	_/ O1	



Raw Sequence Listing

24																
55	(i)	SEQ	UENC	Е СН	ARAC:	rer i	STIC	s:								
56		(A) LE	ngth	: 30	1 am:	ino i	acid	s							
57		(B) TY	PE:	amin	o ac	id									
58		(D) TO	POLO	GY:	line	ar									
59																
60	(ii)	MOL	ECUL	E TY	PE: 1	prot	ein									
61																
62	(iii)	HYP	OTHE:	TICA	L: N	0										
63																
64	(vi)	ORI	GINA	L SO	URCE	:										
65		(A) OR	GANI	SM: Z	Aspe	rgil:	lus :	flav	us						
66																
67	(vii)	IMM	EDIA:	TE S	OURC	E:										
68		(B) CL	ONE:	Ura	te o	xida	se								
69																
70	_															
71	(xi)	SEQ	UENC	E DE	SCRII	PTIO	N: S	EQ I	D NO	:1:						
72		_														
73		Ala	Val	Lys	_	Ala	Arg	Tyr	Gly		Asp	Asn	Val	Arg		Tyr
74	1				5					10					15	
75	_			_	_				_	_	_					
76	Lys	Val	His		Asp	Glu	Lys	Thr		Val	Gln	Thr	Val		Glu	Met
77				20					25					30		
78			_	•	_	_							_	_		
79	Thr	Val		Val	Leu	Leu	Glu		Glu	Ile	Glu	Thr		Tyr	Thr	Lys
80			35					40					45			
81							•			_	_		_	_		
82	AIA	Asp	Asn	ser	VAI	IIe		Ala	Thr	Asp	Ser		Lys	Asn	Thr	Ile
83		50					55					60				
84		-1-	m\		• -	-1					_	_		_		
85 86	65	Ile	Thr	ATA	гĀ2		Asn	Pro	VAI	Thr		Pro	GIu	Leu	Phe	_
87	65					70					75					80
88	5a=	71.	T	~1	Mh	***	Db.	71.	~1	T		•	**	-1-	 • -	
89	Ser	Ile	Leu	GTĀ	85	nis	Pne	iie	GIU	_	TYT	Asn	HIS	IIe		ATA
90					03					90					95	
91	7.1 0	His	17 n l	Nen	Tla	Wo l	Cwa	wi.	N	Mars	mb	B	Wat	N	71.	3
92	VIG	птэ	Val	100	116	VAI	Cys	птр	105	TIP	THE	Arg	Met	110	116	Asp
93				100					103					110		
94	Glv	Lys	Pro	His	Pro	His	Ser	Phe	716	Ara	Agn	Sar	Gl.	Gl u	T.ve	A ~~
95	0-1	_,	115				501	120	116	nry	nsp	561	125	GIU	цув	ALG
96								120					123			
97	Asn	Val	Gln	Va 1	Asn	Va 1	Va 1	Glu	Gl v	T.17 Q	G1v	716	Aen	716	T.37 G	Sar
98		130			p	•	135	O_Lu	011	-11 o	011	140	vob	110	Lly 5	261
99												110				
100	Ser	Leu	Ser	Glv	Lev	Thr	Val	Lev	Lve	Ser	Thr	Asn	Ser	Gln	Phe	Trn
101	145			1		150		~	-12		155					160
102																
103	Glv	Phe	Leu	Ara	Asp	Glu	Tvr	Thr	Thr	Lev	Lvs	Glu	Thr	Tro	Asp	Aro
104	3			3	165		-,-			170	_1 -				175	9
105										_, _						
106	Ile	Leu	Ser	Thr	Asp	Val	Asp	Ala	Thr	Tro	Gln	Tro	Lvs	Asn	Phe	Ser
					-					P			-10			~51

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107				180					185					190		
108		_				_				_	_			41_		
109	GIĀ	Leu	Gln	Glu	Val	Arg	Ser		Val	Pro	Lys	Phe	_	Ala	Thr	Trp
110			195					200					205			
111				_				_	_							
112	Ala		Ala	Arg	Glu	Val		Leu	Lys	Thr	Phe		Glu	Asp	Asn	Ser
113		210					215					220				
114						_										
115		Ser	Val	Gln	Ala		Met	Tyr	Lys	Met		Glu	Gln	Ile	Leu	
116	225					230					235					240
117	_								_							_/_
118	Arg	Gln	Gln	Leu		Glu	Thr	Val	Glu	_	Ser	Leu	Pro	Asn	_	His
119					245					250					255	
120			_													
121	Tyr	Phe	Glu		Asp	Leu	Ser	Trp		Lys	Gly	Leu	Gln		Thr	Gly
122				260					265					270		
123	_	_					_									
124	Lys	Asn	Ala	Glu	Val	Phe	Ala		Gln	Ser	Asp	Pro	Asn	Gly	Leu	Ile
125			275					280					285		•	
126	_	_														
127	Lys		Thr	Val	Gly	Arg		Ser	Leu	Lys	Ser		Leu			
128		290					295					300				
129	(2) INFO	RMAT	ION	FOR S	SEQ :	ED NO	0:2:									
130								_								
131	(1)		UENC								•					
132) LEI					acid	3							
133		•				aci										
134		(C) STI	RANDI	EDNE	SS: 8	sing	le								
134 135		(C		RANDI	EDNE	SS: 8	sing	Le								
134 135 136	/## \	(C (D) STI) TOI	RANDI POLOG	EDNES 3Y:]	SS: s lines	sing! ar	le								
134 135 136 137	(ii)	(C (D) STI) TOI	RANDI POLOG	EDNES 3Y:]	SS: s lines	sing! ar	le								
134 135 136 137 138		(C (D)) STI) TOI ECULI	RANDI POLOG E TYI	edne: 3y:] Pe:]	SS: s lines prote	sing! ar	Le								
134 135 136 137 138 139	(ii) (iii)	(C (D)) STI) TOI ECULI	RANDI POLOG E TYI	edne: 3y:] Pe:]	SS: s lines prote	sing! ar	Le				·				
134 135 136 137 138 139 140	(iii)	(C (D) MOLI) STI) TOI ECULI	RANDI POLO E TYI FICAL	ednes 3Y:] PE:] L: NO	SS: s lines prote	sing! ar	Le								
134 135 136 137 138 139 140		(C (D) MOLI HYPO) STI) TOI ECULI OTHE:	RANDI POLOG E TYI FICAL L SOI	EDNE: 3Y:] PE:] L: NO JRCE:	SS: s lines prote	sing: ar ein					·				
134 135 136 137 138 139 140 141	(iii)	(C (D) MOLI HYPO) STI) TOI ECULI	RANDI POLOG E TYI FICAL L SOI	EDNE: 3Y:] PE:] L: NO JRCE:	SS: s lines prote	sing: ar ein		flavi	18						
134 135 136 137 138 139 140 141 142	(iii) (vi)	(C (D) MOLI HYP(ORI((A)	OTHES	RANDI POLOG E TYI FICAI L SOU GANIS	EDNE: GY:] PE:] L: NO JRCE: SM:]	SS: s lines prote	sing: ar ein		flavı	ıs						
134 135 136 137 138 139 140 141 142 143	(iii)	(C (D) MOLI HYPO ORIO (A)) STI) TOI ECULI OTHE: GINAI) ORG	RANDI POLOG E TYI FICAI L SOI BANIS	EDNE: PE: L: NO JRCE: SM:	SS: : Lines prote Aspen	sing: ar ein	lus 1		18						
134 135 136 137 138 139 140 141 142 143 144	(iii) (vi)	(C (D) MOLI HYPO ORIO (A)	OTHES	RANDI POLOG E TYI FICAI L SOI BANIS	EDNE: PE: L: NO JRCE: SM:	SS: : Lines prote Aspen	sing: ar ein	lus 1		ıs		·				
134 135 136 137 138 139 140 141 142 143 144 145	(iii) (vi)	(C (D) MOLI HYPO ORIO (A)) STI) TOI ECULI OTHE: GINAI) ORG	RANDI POLOG E TYI FICAI L SOI BANIS	EDNE: PE: L: NO JRCE: SM:	SS: : Lines prote Aspen	sing: ar ein	lus 1		ıs						
134 135 136 137 138 139 140 141 142 143 144 145 146	(iii) (vi) (vii)	(C (D) MOLI HYPO ORIC (A) IMMI (B)	OTHE: GINAI ORG	RANDI POLOG E TYI FICAL L SOI BANIS TE SO	EDNES SY: 1 PE: 1 L: NO JRCE: SM: 1 DURCE Met-	SS: s lines prote Aspen	sing: ar sin	lus :	se							
134 135 136 137 138 139 140 141 142 143 144 145 146 147 148	(iii) (vi)	(C (D) MOLI HYPO ORIO (A) IMMI (B)	OTHE: GINAI ORG	RANDI POLOG E TYI FICAL L SOI BANIS TE SO	EDNES SY: 1 PE: 1 L: NO JRCE: SM: 1 DURCE Met-	SS: s lines prote Aspen	sing: ar sin	lus :	se							
134 135 136 137 138 139 140 141 142 143 144 145 146 147 148	(iii) (vi) (vii)	MOLI HYPO ORIO (A) IMMI (B)	OTHE: GINAL ORGE EDIA: OCLO UENCI	RANDI POLOG E TYI FICAL L SOU GANIS TE SO DNE:	EDNES SY: 1 PE: 1 L: NO JRCE: SM: 1 DURCE Met-	SS: : lines prote Aspen L: -Urat	sing ar sin egill	lus i cidas	se O NO:	:2:	Ta		D	v-1	3	Vo.1
134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150	(iii) (vi) (vii) (xi) Met	MOLI HYPO ORIO (A) IMMI (B)	OTHE: GINAI ORG	RANDI POLOG E TYI FICAL L SOU GANIS TE SO DNE:	EDNES GY: 1 PE: 1 L: NO JRCE: SM: 1 DURCE Met- SCRII Lys	SS: : lines prote Aspen L: -Urat	sing ar sin egill	lus i cidas	se O NO:	:2: Gly	Lys	Asp	Asn	Val		Val
134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151	(iii) (vi) (vii)	MOLI HYPO ORIO (A) IMMI (B)	OTHE: GINAL ORGE EDIA: OCLO UENCI	RANDI POLOG E TYI FICAL L SOU GANIS TE SO DNE:	EDNES SY: 1 PE: 1 L: NO JRCE: SM: 1 DURCE Met-	SS: : lines prote Aspen L: -Urat	sing ar sin egill	lus i cidas	se O NO:	:2:	Lys	Asp	Asn	Val	Arg 15	Val
134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151	(iii) (vi) (vii) (xi) Met	MOLI HYPO ORIO (A) IMMI (B) SEQU	OTHES GINAL ORG EDIAS CLG UENCI	RANDI POLOG E TYI FICAL L SOU GANIS CE SC DNE:	EDNES GY: 1 PE: 1 L: NC IRCE: SM: 1 DURCE Met- SCRII Lys 5	SS: : lines prote Aspen C: -Urat PTION Ala	sing ar ein egili te ox	lus : xida: EQ II Arg	e O NO: Tyr	:2: Gly 10	_	_			15	
134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153	(iii) (vi) (vii) (xi) Met	MOLI HYPO ORIO (A) IMMI (B) SEQU	OTHE: GINAL ORGE EDIA: OCLO UENCI	RANDI POLOG E TYI FICAL L SOU JANIS CE SC ONE: Val	EDNES GY: 1 PE: 1 L: NC IRCE: SM: 1 DURCE Met- SCRII Lys 5	SS: : lines prote Aspen C: -Urat PTION Ala	sing ar ein egili te ox	lus : xida: EQ II Arg	e O NO: Tyr Thr	:2: Gly 10	_	_		Val	15	
134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154	(iii) (vi) (vii) (xi) Met	MOLI HYPO ORIO (A) IMMI (B) SEQU	OTHES GINAL ORG EDIAS CLG UENCI	RANDI POLOG E TYI FICAL L SOU GANIS CE SC DNE:	EDNES GY: 1 PE: 1 L: NC IRCE: SM: 1 DURCE Met- SCRII Lys 5	SS: : lines prote Aspen C: -Urat PTION Ala	sing ar ein egili te ox	lus : xida: EQ II Arg	e O NO: Tyr	:2: Gly 10	_	_			15	
134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155	(iii) (vi) (vii) (xi) Met 1	MOLI HYPO ORIO (A) IMMI (B) SEQU Ser	OTHE: GINAL OTHE:	RANDI POLOG E TYI FICAL L SOU JANIS CE SC ONE: Val	EDNES GY:] PE: I L: NC JRCE: SM: / OURCE Met- SCRII Lys Lys	SS: Slines prote prote Aspen Ala Asp	sing ar ein egili ce on H: SI Ala	lus : cidas EQ II Arg	Tyr Thr	:2: Gly 10 Gly	Val	Gln	Thr	Val 30	15 Tyr	Glu
134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156	(iii) (vi) (vii) (xi) Met 1	MOLI HYPO ORIO (A) IMMI (B) SEQU Ser	OTHE: OTHE: GINAL OCIO CLO UENCI Ala Val	RANDI POLOG E TYI FICAL L SOU JANIS CE SC ONE: Val	EDNES GY:] PE: I L: NC JRCE: SM: / OURCE Met- SCRII Lys Lys	SS: Slines prote prote Aspen Ala Asp	sing ar ein egili ce on H: SI Ala	lus : cida: EQ II Arg Lys	Tyr Thr	:2: Gly 10 Gly	Val	Gln	Thr Thr	Val 30	15 Tyr	Glu
134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156	(iii) (vi) (vii) (xi) Met 1	MOLI HYPO ORIO (A) IMMI (B) SEQU Ser	OTHE: GINAL OTHE:	RANDI POLOG E TYI FICAL L SOU JANIS CE SC ONE: Val	EDNES GY:] PE: I L: NC JRCE: SM: / OURCE Met- SCRII Lys Lys	SS: Slines prote prote Aspen Ala Asp	sing ar ein egili ce on H: SI Ala	lus : cidas EQ II Arg	Tyr Thr	:2: Gly 10 Gly	Val	Gln	Thr	Val 30	15 Tyr	Glu
134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156	(iii) (vi) (vii) (xi) Met 1 Tyr	MOLI HYPO ORIO (A) IMMI (B) SEQUENCE LYS	OTHE: OTHE: GINAL OCIO CLO UENCI Ala Val	RANDI POLOG E TYI FICAL L SOU SANIS CE SC ONE: Val His 20 Cys	EDNES GY: 1 PE: 1 L: NO JRCE: SM: 1 DURCE Met- SCRII Lys Lys Val	SS: Slines prote prote Aspen Tion Ala Asp	sing ar sin cgill ce or N: SI Ala Glu	lus s xidas EQ II Arg Lys Glu 40	Tyr Thr 25	:2: Gly 10 Gly Glu	Val	Gln Glu	Thr Thr 45	Val 30 Ser	15 Tyr Tyr	Glu Thr

160			50					55					60				
161																	
162			Tyr	Ile	Thr	Ala	Lys	G1n	Asn	Pro	Val	Thr	Pro	Pro	Glu	Leu	
163	6	5					70					75					80
164																	
165	G	ly	Ser	Ile	Leu	Gly	Thr	His	Phe	Ile			Tyr	Asn	His	Ile	His
166						85					90	٠٠ .				95	
167																	
168	A	la	Ala	His		Asn	Ile	Val	Cys		Arg	Trp	Thr	Arg	Met	Asp	Ile
169					100					105					110		
170																	
171	A	sp	Gly	_	Pro	His	Pro	His	Ser	Phe	Ile	Arg	Asp	Ser	Glu	Glu	Lys
172				115					120					125			
173																	
174	A	rg	Asn	Val	Gln	Val	Asp	Val	Val	Glu	Gly	Lys	Gly	Ile	Asp	Ile	Lys
175			130					135					140				
176																	
177			Ser	Leu	Ser	Gly		Thr	Val	Leu	Lys	Ser	Thr	Asn	Ser	Gln	
178	1	45					150					155					160
179																	
180	T	rp	Gly	Phe	Leu	_	Asp	Glu	Tyr	Thr		Leu	Lys	Glu	Thr	Trp	Asp
181						165					170					175	
182																	
183	A	rg	Ile	Leu		Thr	Asp	Val	Asp	Ala	Thr	Trp	Gln	Trp	Lys	Asn	Phe
184					180					185					190		
185																	
186	S	er	Gly		Gln	Glu	Val	Arg		His	Val	Pro	Lys	Phe	Asp	Ala	Thr
187				195					200					205			
188																	
189	T	rp		Thr	Ala	Arg	Glu		Thr	Leu	Lys	Thr	Phe	Ala	Glu	Asp	Asn
190			210					215					220				
191	_			_				_									
192			Ala	Ser	Val	Gln		Thr	Met	Tyr	Lys		Ala	Glu	Gln	Ile	
193	2	25					230					235					240
194	_	_	_			_											
195	A	Ia	Arg	GIn	GIn		Ile	Glu	Thr	Val		Tyr	Ser	Leu	Pro		Lys
196						245					250					255	
197			_				_	_	_	_		_		_			
198	н	15	Tyr	Phe		Ile	Asp	Leu	Ser		His	Lys	Gly	Leu		Asn	Thr
199					260					265					270		
200	_		_	_						_		_	_	_	_		_
201	G	тА	Lys		ALA	GIu	Val	Phe		Pro	Gln	Ser	Asp	Pro	Asn	Gly	Leu
202				275					280					285			
203	_		_	_				_	_	_	_	_		_			
204	1	Te		CAR	Tnr	VAI	GTĀ	_	Ser	Ser	Leu	Lys		Lys	Leu		
205			290					295					300				
206	/2:	E		-		.ma -											
207	(2) IN	ror	MAT'	ON E	OR S	EQ 1	DN):3:									
208		٠.	CPAT	reara-		D 7 4 4	10P										
209	(ı)	_					STICS									
210								e pa	ıırs								
211					E: r												
212			(0)	STI	CANDE	UNES	5: 8	ingl	.e								

265

Raw Sequence Listing

10/23/91 11:12:11

213	(D) TOPOLOGY: linear	
214		
215	(ii) MOLECULE TYPE: DNA (genomic)	
216		
217	(vii) IMMEDIATE SOURCE:	
218	(B) CLONE: Preferred sequence for expression in	
219	prokaryotes	
220		
221		
222	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
223		
224 225	ATGTCTGCGG TAAAAGCAGC GCGCTACGGC AAGGACAATG TTCGCGTCTA CAAGGTTCAC	60
226	2200200202 202000000 002020000 020202000 020020	100
227	AAGGACGAGA AGACCGGTGT CCAGACGGTG TACGAGATGA CCGTCTGTGT GCTTCTGGAG	120
228	GGTGAGATTG AGACCTCTTA CACCAAGGCC GACAACAGCG TCATTGTCGC AACCGACTCC	180
229	GOIGNONIIG AGACCICIIA CACCAAGGCC GACAACAGCG ICAIIGICGC AACCGACICC	100
230	ATTAAGAACA CCATTTACAT CACCGCCAAG CAGAACCCCG TTACTCCTCC CGAGCTGTTC	240
231		210
232	GGCTCCATCC TGGGCACACA CTTCATTGAG AAGTACAACC ACATCCATGC CGCTCACGTC	300
233	•	
234	AACATTGTCT GCCACCGCTG GACCCGGATG GACATTGACG GCAAGCCACA CCCTCACTCC	360
235		
236	TTCATCCGCG ACAGCGAGGA GAAGCGGAAT GTGCAGGTGG ACGTGGTCGA GGGCAAGGGC	420
237		
238	ATCGATATCA AGTCGTCTCT GTCCGGCCTG ACCGTGCTGA AGAGCACCAA CTCGCAGTTC	480
239		
240 241	TGGGGCTTCC TGCGTGACGA GTACACCACA CTTAAGGAGA CCTGGGACCG TATCCTGAGC	540
241	3000300m00 3m00030mm0 0030m00330 33mmm030m0 030m00300 00m000	600
242	ACCGACGTCG ATGCCACTTG GCAGTGGAAG AATTTCAGTG GACTCCAGGA GGTCCGCTCG	600
244	CACGTGCCTA AGTTCGATGC TACCTGGGCC ACTGCTCGCG AGGTCACTCT GAAGACTTTT	660
245	CARDISCOIR AGIICGAIGC IACCIGGGCC ACIGCICGCG AGGICACICI GAAGACIIII	880
246	GCTGAAGATA ACAGTGCCAG CGTGCAGGCC ACTATGTACA AGATGGCAGA GCAAATCCTG	720
247		, 20
248	GCGCGCCAGC AGCTGATCGA GACTGTCGAG TACTCGTTGC CTAACAAGCA CTATTTCGAA	780
249		
250	ATCGACCTGA GCTGGCACAA GGGCCTCCAA AACACCGGCA AGAACGCCGA GGTCTTCGCT	840
251		
252	CCTCAGTCGG ACCCCAACGG TCTGATCAAG TGTACCGTCG GCCGGTCCTC TCTGAAGTCT	900
253		
254	AAATTG	906
255	(8)	
256	(2) INFORMATION FOR SEQ ID NO:4:	
257	(i) SEQUENCE CHARACTERISTICS:	
258 259	(A) LENGTH: 906 base pairs	
260	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
261	(C) STRANDEDNESS: Single (D) TOPOLOGY: linear	
262	(n) Totopogr, Timedi	
263	(ii) MOLECULE TYPE: DNA (genomic)	
264	() ====== ()===== ()	

Raw Sequence Listing

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266 267 268 269	(vii) IMMEDIATE SOURCE:(B) CLONE: Preferred sequence for expression in eukaryotes	
270	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
271	(vr) pakamian appoint from pro in work.	
272 273	ATGTCTGCTG TTAAGGCTGC TAGATACGGT AAGGACAACG TTAGAGTCTA CAAGGTTCAC	60
274 275	AAGGACGAGA AGACCGGTGT CCAGACGGTG TACGAGATGA CCGTCTGTGT GCTTCTGGAG	120
276 277	GGTGAGATTG AGACCTCTTA CACCAAGGCC GACAACAGCG TCATTGTCGC AACCGACTCC	180
278 279	ATTAAGAACA CCATTTACAT CACCGCCAAG CAGAACCCCG TTACTCCTCC CGAGCTGTTC	240
280 281	GGCTCCATCC TGGGCACACA CTTCATTGAG AAGTACAACC ACATCCATGC CGCTCACGTC	300
282 283	AACATTGTCT GCCACCGCTG GACCCGGATG GACATTGACG GCAAGCCACA CCCTCACTCC	360
284 285	TTCATCCGCG ACAGCGAGGA GAAGCGGAAT GTGCAGGTGG ACGTGGTCGA GGGCAAGGGC	420
286 287	ATCGATATCA AGTCGTCTCT GTCCGGCCTG ACCGTGCTGA AGAGCACCAA CTCGCAGTTC	480
288 289	TGGGGCTTCC TGCGTGACGA GTACACCACA CTTAAGGAGA CCTGGGACCG TATCCTGAGC	540
290 291	ACCGACGTCG ATGCCACTTG GCAGTGGAAG AATTTCAGTG GACTCCAGGA GGTCCGCTCG	600
292 293	CACGTGCCTA AGTTCGATGC TACCTGGGCC ACTGCTCGCG AGGTCACTCT GAAGACTTTT	660
294 295	GCTGAAGATA ACAGTGCCAG CGTGCAGGCC ACTATGTACA AGATGGCAGA GCAAATCCTG	720
296 297	GCGCGCCAGC AGCTGATCGA GACTGTCGAG TACTCGTTGC CTAACAAGCA CTATTTCGAA	780
298 299	ATCGACCTGA GCTGGCACAA GGGCCTCCAA AACACCGGCA AGAACGCCGA GGTCTTCGCT	840
300 301	CCTCAGTCGG ACCCCAACGG TCTGATCAAG TGTACCGTCG GCCGGTCCTC TCTGAAGTCT	900
302 303	AAATTG	906
304 305	(2) INFORMATION FOR SEQ ID NO:5:	
306	(i) SEQUENCE CHARACTERISTICS:	
307	(A) LENGTH: 14 base pairs	
308	(B) TYPE: nucleic acid	
309 310	(C) STRANDEDNESS: single	
311	(D) TOPOLOGY: linear	
312	(ii) MOLECULE TYPE: DNA (genomic)	
313	(11) WODECOME TIPE: DAM (AGROWIC)	
314	(iii) HYPOTHETICAL: NO	
315	\	
316		
317	(vii) IMMEDIATE SOURCE:	
318	(B) CLONE: Preferred non-translated 5' sequence for	

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319	animal cells	
320		
321	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
322	AGCTTGCCGC CACT	14
323		
324	(2) INFORMATION FOR SEQ ID NO:6:	
325	,	
326	(i) SEQUENCE CHARACTERISTICS:	
327		
328	(B) TYPE: nucleic acid	
329	(C) STRANDEDNESS: single	
330	(D) TOPOLOGY: linear	
331	(b) Topologi: linear	
332	(ii) NOTEGUTE MUDE: DUR (moneyis)	
	(ii) MOLECULE TYPE: DNA (genomic)	
333 334	(111) TURANTUMTAT. NA	
	(iii) HYPOTHETICAL: NO	
335		
336	(a.11)	
337	(vii) IMMEDIATE SOURCE:	
338	(B) CLONE: Preferred sequence for expression in animal	
339 340	cells	
341		
342	(with appropriate the control of the	
343	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
344	3M0M000030 M333300300 0000M30000 33003033M0 M00000M30000	
345	ATGTCCGCAG TAAAAGCAGC CCGCTACGGC AAGGACAATG TCCGCGTCTA CAAGGTTCAC	60
346	AAGGACGAGA AGACCGGTGT CCAGACGGTG TACGAGATGA CCGTCTGTGT GCTTCTGGAG	100
347	AAGGACGAGA AGACCGGTGT CCAGACGGTG TACGAGATGA CCGTCTGTGT GCTTCTGGAG	120
348	GGTGAGATTG AGACCTCTTA CACCAAGGCC GACAACAGCG TCATTGTCGC AACCGACTCC	180
349	GOIGNONIIG NONCCICIIN CACCANGGCC GACAMCAGCG ICAITGICGC AACCGACTCC	100
350	ATTAAGAACA CCATTTACAT CACCGCCAAG CAGAACCCCG TTACTCCTCC CGAGCTGTTC	240
351	ATTANOANCA CONTITACAT CACCOCCAAG CAGAMCCCCG TIACTCCTCC CGAGCTGTTC	240
352	GGCTCCATCC TGGGCACACA CTTCATTGAG AAGTACAACC ACATCCATGC CGCTCACGTC	300
353	GOCICCATCC IGGGCACACA CIICAIIGAG AAGIACAACC ACAICCAIGC CGCICACGIC	300
354	AACATTGTCT GCCACCGCTG GACCCGGATG GACATTGACG GCAAGCCACA CCCTCACTCC	260
355	AACAIIGICI GCCACCGCIG GACCCCGGAIG GACAIIGACG GCAAGCCACA CCCTCACTCC	360
356	TTCATCCGCG ACAGCGAGGA GAAGCGGAAT GTGCAGGTGG ACGTGGTCGA GGGCAAGGGC	420
357	TICHICCOCO ACAGCOAGGA GAAGCOGAAI GIGCAGGIGG ACGIGGICGA GGGCAAGGGC	420
358	ATCGATATCA AGTCGTCTCT GTCCGGCCTG ACCGTGCTGA AGAGCACCAA CTCGCAGTTC	400
359	ALCONIATION ROLCOTOLICI GICCOGCCIG RCCGIGCIGA RGAGCACCAA CICGCAGIIC	480
360	TGGGGCTTCC TGCGTGACGA GTACACCACA CTTAAGGAGA CCTGGGACCG TATCCTGAGC	EAG
361	199999199 1999194994 SIRCHCCACA CIIAAGGAGA CCIGGGACCG IAICCIGAGC	540
362	ACCGACGTCG ATGCCACTTG GCAGTGGAAG AATTTCAGTG GACTCCAGGA GGTCCGCTCG	600
363		300
364	CACGTGCCTA AGTTCGATGC TACCTGGGCC ACTGCTCGCG AGGTCACTCT GAAGACTTTT	660
365		300
366	GCTGAAGATA ACAGTGCCAG CGTGCAGGCC ACTATGTACA AGATGGCAGA GCAAATCCTG	720
367	nonorocono corococo acinistaca againgcaga gcamatecin	720
368	GCGCGCCAGC AGCTGATCGA GACTGTCGAG TACTCGTTGC CTAACAAGCA CTATTTCGAA	780
369		, 60
370	ATCGACCTGA GCTGGCACAA GGGCCTCCAA AACACCGGCA AGAACGCCGA GGTCTTCGCT	840
371		320

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272	CCICAGICGG ACCCCAACGG ICIGAICAAG IGIACCGICG GCCGGTCCTC TCTGAAGTCT	700
373		
374	AAATTG	906
375		
376	(2) INFORMATION FOR SEQ ID NO:7:	
377		
378	(i) SEQUENCE CHARACTERISTICS:	
379	(A) LENGTH: 23 base pairs	
380	(B) TYPE: nucleic acid	
381	(C) STRANDEDNESS: single	
382	(D) TOPOLOGY: linear	
383	• •	
384	(ii) MOLECULE TYPE: DNA (genomic)	
385	(iii) HYPOTHETICAL: NO	
386	(,	
387		
388	(vii) IMMEDIATE SOURCE:	
389		
390	(B) CLONE: reverse transcription primer	
391		
392	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
393		
394	GATCCGGGCC CTTTTTTTT TTT	23
395		
396	(2) INFORMATION FOR SEQ ID NO:8:	
397		
398	(i) SEQUENCE CHARACTERISTICS:	
399	(A) LENGTH: 10 amino acids	
400	(B) TYPE: amino acid	
401	(C) STRANDEDNESS: single	
402	(D) TOPOLOGY: linear	
403	(-,	
404	(ii) MOLECULE TYPE: peptide	
405	(a) the same of the popular	
406	(iii) HYPOTHETICAL: NO	
407	(III) III OIMBITCAM. NO	
408		
409	(vii) IMMEDIATE SOURCE:	
410		
	(B) CLONE: Hydrolysis product T 17	
411		
412		
413	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
414		
415	Asn Val Gln Val Asp Val Val Glu Gly Lys	
416	1 5 10	
417		
418	(2) INFORMATION FOR SEQ ID NO:9:	
419		
420	(i) SEQUENCE CHARACTERISTICS:	
421	(A) LENGTH: 8 amino acids	
422	(B) TYPE: amino acid	
423	(C) STRANDEDNESS: single	
424	(D) TOPOLOGY: linear	
	\-,	

425		
426	(ii)	MOLECULE TYPE: peptide
427		
428	(iii)	HYPOTHETICAL: NO
429		
430	(V11)	IMMEDIATE SOURCE:
431		(B) CLONE: Hydrolysis product T 20
432 433		
434	(***	SEQUENCE DESCRIPTION: SEQ ID NO:9:
435	(XI)	SEQUENCE DESCRIPTION: SEQ ID NO: 7:
436	Agn	Phe Ser Gly Leu Gln Glu Val
437	1	5
438	•	3
439	(2) INFO	RMATION FOR SEQ ID NO:10:
440	(2, 111101	
441	(i)	SEQUENCE CHARACTERISTICS:
442	` '	(A) LENGTH: 6 amino acids
443		(B) TYPE: amino acid
444		(C) STRANDEDNESS: single
445		(D) TOPOLOGY: linear
446		
447	(ii)	MOLECULE TYPE: peptide
448		
449	(iii)	HYPOTHETICAL: NO
450		
451		
452	(vii)	IMMEDIATE SOURCE:
453		(B) CLONE: Hydrolysis product T 23
454		
455		
456	(XI)	SEQUENCE DESCRIPTION: SEQ ID NO:10:
457	5 1-	Now all who were all
458 459		Asp Ala Thr Trp Ala
460	1	5
461	/2\ TNEOI	PARTICH FOR SEA TO NO. 11.
462	(Z) INFO	RMATION FOR SEQ ID NO:11:
463	(3)	SPONENCE CHARACTERISTICS.
464	(1)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 8 amino acids
465		(B) TYPE: amino acid
466		(C) STRANDEDNESS: single
467		(D) TOPOLOGY: linear
468		(2) 101020011 112001
469	(ii)	MOLECULE TYPE: peptide
470	\ <i>\</i>	· · · · · · · · · · · · · · · · · · ·
471	(iii)	HYPOTHETICAL: NO
472	• ,	
473		
474	(vii)	IMMEDIATE SOURCE:
475		(B) CLONE: Hydrolysis product T 27
476		
477		

```
478
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
479
480
          His Tyr Phe Glu Ile Asp Leu Ser
481
482
483
     (2) INFORMATION FOR SEQ ID NO:12:
484
485
          (i) SEQUENCE CHARACTERISTICS:
486
               (A) LENGTH: 13 amino acids
487
               (B) TYPE: amino acid
488
               (C) STRANDEDNESS: single
489
               (D) TOPOLOGY: linear
490
491
         (ii) MOLECULE TYPE: peptide
492
493
        (iii) HYPOTHETICAL: NO
494
495
496
        (vii) IMMEDIATE SOURCE:
497
               (B) CLONE: Hydrolysis product T 28
498
499
500
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
501
502
          Ile Leu Ser Thr Asp Val Asp Ala Thr Trp Gln Trp Lys
503
504
505
     (2) INFORMATION FOR SEQ ID NO:13:
506
507
          (i) SEQUENCE CHARACTERISTICS:
508
               (A) LENGTH: 11 amino acids
509
               (B) TYPE: amino acid
510
               (C) STRANDEDNESS: single
511
               (D) TOPOLOGY: linear
512
513
         (ii) MOLECULE TYPE: peptide
514
515
        (iii) HYPOTHETICAL: NO
516
517
518
        (vii) IMMEDIATE SOURCE:
519
               (B) CLONE: Hydrolysis product T 29
520
521
522
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
523
524
          His Tyr Phe Glu Ile Asp Leu Ser Trp His Lys
525
                                                10
526
527
     (2) INFORMATION FOR SEQ ID NO:14:
528
529
          (i) SEQUENCE CHARACTERISTICS:
530
               (A) LENGTH: 11 amino acids
```

231		(B) TYPE: amino acid
532		(C) STRANDEDNESS: single
533		(D) TOPOLOGY: linear
534		
535	(ii)	MOLECULE TYPE: peptide
536	• • •	
537	(iii)	HYPOTHETICAL: NO
538	(,	
539		
540	(vii)	IMMEDIATE SOURCE:
541	(/	(B) CLONE: Hydrolysis product T 31
542		(b) about highest product 1 31
543		
544	(vi)	SEQUENCE DESCRIPTION: SEQ ID NO: 14:
545	(71)	Degrade Description. Shy is notife
546	Ser	Thr Asn Ser Gln Phe Trp Gly Phe Leu Arg
547	1	
548	•	5 10
549	(2) TNEO	RMATION FOR SEQ ID NO:15:
550	(2) INFO	RMATION FOR SEQ ID NO:13:
551	/: \	SEQUENCE CHARACTERISTICS:
552	(1)	(A) LENGTH: 16 amino acids
553		(B) TYPE: amino acid
554		(C) STRANDEDNESS: single
555		(C) STRANDEDNESS: SINGLE (D) TOPOLOGY: linear
556		(b) TOPOLOGI: Timear
557	/::>	MOT POIL P MVDP . montide
558	(11)	MOLECULE TYPE: peptide
559	1222	HUBOMUMTALT. NO
560	(111)	HYPOTHETICAL: NO
561		
562	4	
563	(411)	IMMEDIATE SOURCE:
		(B) CLONE: Hydrolysis product T 32
564		
565	4	
566	(XI)	SEQUENCE DESCRIPTION: SEQ ID NO:15:
567	63 .	
568		Asn Pro Val Thr Pro Pro Glu Leu Phe Gly Ser Ile Leu Gly Thr
569	1	5 10 15
570		
571		
572	(2) INFO	RMATION FOR SEQ ID NO:16:
573		
574	(i)	SEQUENCE CHARACTERISTICS:
575		(A) LENGTH: 16 amino acids
576		(B) TYPE: amino acid
577		(C) STRANDEDNESS: single
578		(D) TOPOLOGY: linear
579		
580	(ii)	MOLECULE TYPE: peptide
581		
582	(iii)	HYPOTHETICAL: NO
583	•	

584		
585	(vii)	IMMEDIATE SOURCE:
586		(B) CLONE: Hydrolysis product T 33
587		
588		
589	(x1)	SEQUENCE DESCRIPTION: SEQ ID NO:16:
590		
591		Asn Pro Val Thr Pro Pro Glu Leu Phe Gly Ser Ile Leu Gly Thr
592	1	5 10 15
593		
594	/0\ TYPO	DUBETON FOR AND TO MALER
595	(2) INFO	RMATION FOR SEQ ID NO:17:
596 507	445	
597	(1)	SEQUENCE CHARACTERISTICS:
598		(A) LENGTH: 25 amino acids
599		(B) TYPE: amino acid
600		(C) STRANDEDNESS: single
601 602		(D) TOPOLOGY: linear
603	122	NOT BOTT III MYDIN
604	(11)	MOLECULE TYPE: peptide
605	/:::\	HYPOTHETICAL: NO
606	(111)	HIPOTRETICAL: NO
607		
608	/ii\	IMMEDIATE SOURCE:
609	(*11)	
610		(B) CLONE: Hydrolysis product V 1
611		
612	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:17:
613	(11)	Digustics Discritition. Shy ID NO.17.
614	Tur	Ser Leu Pro Asn Lys Ala Asp Asn Ser Val Ile Val Asp Thr Asp
615	1	5 10 15
616	-	3 10 13
617	Ser	Ile Lys Asn Thr Ile Tyr Ile Thr
618		20 25
619		25
620	(2) INFO	RMATION FOR SEQ ID NO:18:
621	\-,	
622	(i)	SEQUENCE CHARACTERISTICS:
623	• • •	(A) LENGTH: 16 amino acids
624		(B) TYPE: amino acid
625		(C) STRANDEDNESS: single
626		(D) TOPOLOGY: linear
627		
628	(ii)	MOLECULE TYPE: peptide
629		
630	(iii)	HYPOTHETICAL: NO
631	•	
632		
633	(vii)	IMMEDIATE SOURCE:
634		(B) CLONE: Hydrolysis product V 2
635		
636		

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63/	(XI)	SEQUENCE DESCRIPTION: SEQ ID NO:18:
638		
639	Val	Thr Leu Lys Thr Phe Ala Glu Asp Asn Ser Ala Ser Val Gln Ala
640	1	5 10 15
641		
642	(2) INFO	RMATION FOR SEQ ID NO:19:
643	(-,	
644	(i)	SEQUENCE CHARACTERISTICS:
645	\-/	(A) LENGTH: 24 amino acids
646		(B) TYPE: amino acid
647		(C) STRANDEDNESS: single
648		(D) TOPOLOGY: linear
649		(b) lorohodi: lineal
650	/::\	NOT FOUR E MYDE:
651	(11)	MOLECULE TYPE: peptide
	,,,,,	HUDAHUMATALI. MA
652	(111)	HYPOTHETICAL: NO
653		
654		
655	(Vii)	IMMEDIATE SOURCE:
656		(B) CLONE: Hydrolysis product V 3
657		
658		
659	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:19:
660		
661	Thr	Ser Tyr Thr Lys Ala Asp Asn Ser Val Ile Val Asp Thr Asp Ser
662	1	5 10 15
663		
664	Ile	Lys Asn Thr Ile Tyr Ile Thr
665		20
666		
667	(2) INFO	RMATION FOR SEQ ID NO:20:
668		
669	(i)	SEQUENCE CHARACTERISTICS:
670		(A) LENGTH: 28 amino acids
671		(B) TYPE: amino acid
672		(C) STRANDEDNESS: single
673		(D) TOPOLOGY: linear
674		
675	(ii)	MOLECULE TYPE: peptide
676	` '	
677	(iii)	HYPOTHETICAL: NO
678	\/	
679		
680	(vii)	IMMEDIATE SOURCE:
681	(****	(B) CLONE: Hydrolysis product V 5
682		(2) among, njaronjene product v 3
683		
684	(vi)	SEQUENCE DESCRIPTION: SEQ ID NO:20:
685	(~=)	
686	al	Lys Gly Ile Asp Ile Lys Ser Ser Leu Ser Gly Leu Thr Val Leu
687	1	
688	1	5 10 15
689	T	Sow Mhy Ann Con Cla Dhe Man Clar Dhe To The Control of the Control
907	гÃг	Ser Thr Asn Ser Gln Phe Trp Gly Phe Leu Arg

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690		20	25		
691					
692	(2) INFO	RMATION FOR SEQ ID NO:21	.:		
693					
694	(i)	SEQUENCE CHARACTERISTIC	s:		
695		(A) LENGTH: 17 amino a	cids		
696		(B) TYPE: amino acid			
697		(C) STRANDEDNESS: sing	rle		
698		(D) TOPOLOGY: linear	,		
699		(2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2			
700	(ii)	MOLECULE TYPE: peptide			
701	()	mean and a second			
702	(1111)	HYPOTHETICAL: NO			
703	(111)	mii olindilong. No			
704					
705	(mii)	IMMEDIATE SOURCE:			
706	(411)		and the		
707		(B) CLONE: Hydolysis p	product v 6		
708					
708 709	445				
710	(XI)	SEQUENCE DESCRIPTION: S	EQ ID NO:21:		
	61	T 61 71- 7 71- 7			
711		Lys Gly Ile Asp Ile Lys			
712	1	5	10	15	
713	_				
714	Lys				
715					
716	_				
717	(2) INFO	RMATION FOR SEQ ID NO:22	:		
718					
719	(i)	SEQUENCE CHARACTERISTIC			
720		(A) LENGTH: 1236 base	_		
721		(B) TYPE: nucleic acid			
722		(C) STRANDEDNESS: sing	le		
723		(D) TOPOLOGY: linear			
724					
725	(ii)	MOLECULE TYPE: DNA (gen	omic)		
726					
727	(iii)	HYPOTHETICAL: NO			
728					
729					
730	(vii)	IMMEDIATE SOURCE:			
731	` ,	(B) CLONE: Fragment 3			
732		• •			
733					
734	(xi)	SEQUENCE DESCRIPTION: S	EO ID NO:22:		
735	(**-)	g			
736	GATCCGCG	GA AGCATAAAGT GTAAAGCCTG	GGGTGCCTAA TGAGTGA	ርርጥ አልርጥጥልሮልጥጥ	60
737	2 30000	OIMMOULU	TOTOGOLIM TONGTON	nnvaanvnaa	00
738	ልልጥጥርርርሙ	TG CGCTCACTGC CCGCTTTCCA	GTCGGGAAAC CTGTCGT	<u>ር</u> ርር አርርጥርርአጥጥአ	120
739		TO COULDING COURTILLOW	CICGGANAC CIGICGI	ACC VOCTOCATIA	12(
740	አጥርያ አጥርር	GC CAACGCGCGG GGAGAGGCGG	TTTTCCCTATT CCCCCCC		10/
741	HIGHNICH	SC CARCUCUCUG GGAGAGGCGG	IIIGCGTATT GGGCGCC	MGG GTGGTTTTTC	180
742	መመመመረ አረረ ነ	NO TONONOCOCO NACROSTO	TO COOTTO A COOTTO	000 000000000	244
144	TTTTCACC	AG TGAGACGGGC AACAGCTGAT	TOCCCTTUAC CGCCTGG	CCC TGAGAGAGTT	240

795

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743							
744	GCAGCAAGCG	GTCCACGCTG	GTTTGCCCCA	CCACCCGAAA	ATCCTGTTTG	ATGGTGGTTA	300
745							
746	ACGGCGGGAT	ATAACATGAG	CTGTCTTCGG	TATCGTCGTA	TCCCACTACC	GAGATATCCG	360
747							
748	CACCAACGCG	CAGCCCGGAC	TCGGTAATGG	CGCGCATTGC	GCCCAGCGCC	ATCTGATCGT	420
749							
750	TGGCAACCAG	CATCGCAGTG	GGAACGATGC	CCTCATTCAG	CATTTGCATG	GTTTGTTGAA	480
751							
752 753	AACCGGACAT	GGCACTCCAG	TCGCCTTCCC	GTTCCGCTAT	CGGCTGAATT	TGATTGCGAG	540
754	ጥርልርልጥልጥጥጥ	ATGCCAGCCA	GCCAGACGCA	GACGCGCCGA	CACACAACDO	NAME COCCO	600
755	TOHORITALI	HICCHOCCA	GCCHGACGCA	GACGCGCCGA	GACAGAACII	ANIGGGCCCG	800
756	CTAACAGCGC	GATTTGCTGG	TGACCCAATG	CGACCAGATG	CTCCACGCCC	AGTCGCGTAC	660
757							
758	CGTCTTCATG	GGAGAAAATA	ATACTGTTGA	TGGGTGTCTG	GTCAGAGACA	TCAAGAAATA	720
759							
760	ACGCCGGAAC	ATTAGTGCAG	GCAGCTTCCA	CAGCAATGGC	ATCCTGGTCA	TCCAGCGGAT	780
761							
762	AGTTAATGAT	CAGCCCACTG	ACGCGTTGCG	CGAGAAGATT	GTGCACCGCC	GCTTTACAGG	840
763 764	CDTCC NCCCC	GCTTCGTTCT	N.C.C.S.M.C.C.S.C.S.	CC1 CC1 CCC	000300030m	ma>maaaaa	000
765	CIICGACGCC	GCTTCGTTCT	ACCATCGACA	CCACCACGCT	GGCACCCAGT	TGATCGGCGC	900
766	GAGATTTAAT	CGCCGCGACA	ATTTGCGACG	GCGCGTGCAG	GGCCAGACTG	GAGGTGGCAA	960
767					0000110110110	Olioo1000ili	700
768	CGCCAATCAG	CAACGACTGT	TTGCCCGCCA	GTTGTTGTGC	CACGCGGTTG	GGAATGTAAT	1020
769	TCAGCTCCGC	CATCGCCGCT	TCCACTTTTT	CCCGCGTTTT	CGCAGAAACG	TGGCTGGCCT	1080
770							
771	GGTTCACCAC	GCGGGAAACG	GTCTGATAAC	AGACACCGGC	ATACTCTGCG	ACATCGTATA	1140
772							
773 774	ACGITACIGG	TTTCACATTC	ACCACCCTGA	ATTGACTCTC	TTCCGGGCGC	TATCATGCCA	1200
775	TACCGCGAAA	GGTTTTGCGC	CATTCCATCC	TOTO CO			1236
776	Incodedam	GGIIIIGCGC	CATICGAIGG	IGICCG			1236
777	(2) INFORMA	ATION FOR SE	EO ID NO:23	1			
778	(-,						
779	(i) SI	EQUENCE CHAP	RACTERISTICS	5:			
780		(A) LENGTH:	326 base pa	airs			
781		(B) TYPE: nu	cleic acid				
782	•	(C) STRANDEL	NESS: singl	le			
783	•	(D) TOPOLOGY	: linear				
784	4335 20						
785 786	(11) MC	OLECULE TYPE	: DNA (gend	owrc)			
787	(iii) HY	YPOTHETICAL:	NO				
788	(~~~) 11.	vimilonii	410				
789							
790	(vii) IN	MEDIATE SOU	IRCE:				
791	•	(B) CLONE: F					
792					•		
793							
794	(xi) SE	EQUENCE DESC	RIPTION: SE	Q ID NO:23:	}		

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796	TCGAGCTGAC TGACCTGTTG CTTATATTAC ATCGATAGCT TAGCGTATAA TGTGTGGAAT	60						
797								
798	TGTGAGCGAT AACAATTTCA CACAGTTTAA CTTTAAGAAG GAGATATACA TATGGCTACC	120						
799								
800	GGATCCCGGA CTAGTCTGCT CCTGGCTTTT GGCCTGCTCT GCCTGCCCTG GCTTCAAGAG	180						
801								
802	GGCAGTGCCT TCCCAACCAT TCCCTTATCT AGACTTTTTG ACAACGCTAT GCTCCGCGCC	240						
803								
804	CATCGTCTGC ACCAGCTGGC CTTTGACACC TACCAGGAGT TTGAAGAAGC CTATATCCCA	300						
805	AAGGAACAGA AGTATTCATT CCTGCA	326						
806								
807	(2) INFORMATION FOR SEQ ID NO:24:							
808								
809	(i) SEQUENCE CHARACTERISTICS:							
810	(A) LENGTH: 74 base pairs							
811	(B) TYPE: nucleic acid							
812	(C) STRANDEDNESS: single	•						
813	(D) TOPOLOGY: linear							
814								
815	(ii) MOLECULE TYPE: DNA (genomic)							
816								
817	(iii) HYPOTHETICAL: NO							
818								
819								
820	(vii) IMMEDIATE SOURCE:							
821	(B) CLONE: ClaI-NdeI fragment							
822								
823								
824	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:							
825								
826	CGATAGCGTA TAATGTGTGG AATTGTGAGC GGATAACAAT TTCACACAGT TTTTCGCGAA	60						
827		•						
828	GAAGGAGATA TACA 74							
829								
830	(2) INFORMATION FOR SEQ ID NO:25:							
831								
832	(i) SEQUENCE CHARACTERISTICS:							
833	(A) LENGTH: 163 base pairs							
834	(B) TYPE: nucleic acid							
835	(C) STRANDEDNESS: single							
836	(D) TOPOLOGY: linear							
837	(2) 101 020011 112001							
838	(ii) MOLECULE TYPE: DNA (genomic)							
839	(11) NORDOURD IIIB. DNA (GENOMIC)							
840	(iii) HYPOTHETICAL: NO							
841	(111) HIPOINDIIGAD: NO							
842								
843	(vii) IMMEDIATE SOURCE:							
844	(VII) IMMEDIATE SOURCE: (B) CLONE: Synthetic hGH gene end fragment							
845	(a) chous: Synthetic non dene end iragment							
846								
847	(vi) CENTENCE DECEDEDATON. CEN TO NO.25.							
848	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:							
0.50								

Raw Sequence Listing

10/23/91 11:13:34

849 850	GATCTTCAAG CAGACCTACA GCGACGCACT ACTCAAGAAC TACGGGCTGC TCTACTGCTT	60
851	CAGGAAGGAC ATGGACAAGG TCGAGACATT CCTGCGCATC GTGCAGTGCC GCTCTGTGGA	100
852	CAGGAAGGAC AIGGACAAGG ICGAGACAIT CCIGCGCATC GIGCAGIGCC GCICTGIGGA	120
853	GGGCAGCTGT GGCTTCTAGT AAGGTACCCT GCCCTACGTA CCA	163
854	GGGCAGCIGI GGCIICIAGI AAGGIACCCI GCCCTACGIA CCA	163
855	(2) INFORMATION FOR SEO ID NO:26:	
856	(2) INFORMATION FOR SEQ ID NO: 20:	
857	(i) SEQUENCE CHARACTERISTICS:	
858	(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 base pairs	
859	(B) TYPE: nucleic acid	
860	• •	
861	(C) STRANDEDNESS: single	
862	(D) TOPOLOGY: linear	
863	(ii) NOT EGIT E MUDE, DAY (concein)	
864	(ii) MOLECULE TYPE: DNA (genomic)	
865	/::\ HUDOMHEMTORT. NO	
866	(iii) HYPOTHETICAL: NO	
867		
868	(vii) IMMEDIATE SOURCE:	
869	(VII) IMMEDIATE SOURCE: (B) CLONE: NdeI-AccII synthetic fragment	
870	(b) CLORE: Mdel-Accil synthetic fragment	
871		
872	(xi) SEQUENCE DESCRIPTION: SEO ID NO:26:	
873	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
874	TATGTCTGCG GTAAAAGCAG CGCGCTACGG CAAGGACAAT GTTCGCGT	40
875	INIGICIOCO GIANAMOCAG COCGCIACOG CAMOGACANI GIICGCGI	48
876	(2) INFORMATION FOR SEQ ID NO:27:	
877	(2) INFORMATION FOR SEQ ID NO:27;	
878	(i) SEQUENCE CHARACTERISTICS:	
879	(A) LENGTH: 361 base pairs	
880	(B) TYPE: nucleic acid	
881	(C) STRANDEDNESS: single	
882	(D) TOPOLOGY: linear	
883	(b) 10.02001. IIacal	
884	(ii) MOLECULE TYPE: DNA (genomic)	
885	(11) Nondound III I. Dan (genomic)	
886	(iii) HYPOTHETICAL: NO	
887	(222) 211 022220221. 110	
888		
889	(vii) IMMEDIATE SOURCE:	
890	(B) CLONE: Plasmid pEMR469 fragment with ADH2 promoter	
891	(2) CLOND: ! labmid phintery liagment with ADN2 promoter	
892		
893	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:	
894	("") DIGULACE DESCRIPTION. DEG ID NO.2/;	
895	GGGACGCGTC TCCTCTGCCG GAACACCGGG CATCTCCAAC TTATAAGTTG GAGAAATAAG	60
896		90
897	AGAATTTCAG ATTGAGAGAA TGAAAAAAAA AAAAAAAAAA	120
898	MANIATOR OCCUPANTA CONTINUAL CONTINU	120
899	AATGGGGTTC ACTTTTTGGT AAAGCTATAG CATGCCTATC ACATATAAAT AGAGTGCCAG	180
900	DAJJULDADA IRANIALIANA SIRIUSURAN DALGUELANA ELECTRICA CARRESTANDO DE CONTRACTOR DE CO	100
901	TAGCGACTIT TITCACACTC GAGATACTCT TACTACTGCT CTCTTGTTGT TTTTATCACT	240

Raw Sequence Listing

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902		
903	TCTTGTTTCT TCTTTGGTAA ATAGAATATC AAGCTACAAA AAGCATACAA TCAACTATCA	300
904		300
905	ACTATTAACT ATATCGATAC CATATGGATC CGTCGACTCT AGAGGATCGT CGACTCTAGA	360
906	ACIALIANCE ALAICONIAC CALAIGONIC COICONCICE AGAGGAICGE CONCICIAGA	300
907	G ·	361
908	G	361
909	(2) THEODISMICH FOR CEO IN NO. 20.	
910	(2) INFORMATION FOR SEQ ID NO:28:	
911	() CENTENCE AND COURT OF ACT	
	(i) SEQUENCE CHARACTERISTICS:	
912	(A) LENGTH: 58 base pairs	
913	(B) TYPE: nucleic acid	
914	(C) STRANDEDNESS: single	
915	(D) TOPOLOGY: linear	
916		
917	(ii) MOLECULE TYPE: DNA (genomic)	
918		
919	(iii) HYPOTHETICAL: NO	
920		
921		
922	(vii) IMMEDIATE SOURCE:	
923	(B) CLONE: Fragment C	
924		
925		
926	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:	
927		
928	CGATATACAC AATGTCTGCT GTTAAGGCTG CTAGATACGG TAAGGACAAC GTTAGAGT	58
929		
930	(2) INFORMATION FOR SEQ ID NO: 29:	
931		
932	(i) SEQUENCE CHARACTERISTICS:	
933	(A) LENGTH: 1013 base pairs	
934	(B) TYPE: nucleic acid	
935	(C) STRANDEDNESS: single	
936	(D) TOPOLOGY: linear	
937		
938	(ii) MOLECULE TYPE: DNA (genomic)	
939		
940	(iii) HYPOTHETICAL: NO	
941		
942		
943	(vii) IMMEDIATE SOURCE:	
944	(B) CLONE: Fragment D	
945		
946		
947	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:	
948		
949	CTACAAGGTT CACAAGGACC ACAAGACCGG TGTCCAGACG GTGTACGAGA TGACCGTCTG	60
950		
951	TGTGCTTCTG GAGGGTGAGA TTGAGACCTC TTACACCAAG GCCGACAACA GCGTCATTGT	120
952		
953	CGCAACCGAC TCCATTAAGA ACACCATTTA CATCACCGCC AAGCAGAACC CCGTTACTCC	180
954		

1007

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955 956	TCCCGAGCTG TTCGGCTCCA TCCTGGGCAC ACACTTCAT TGAGAAGTAC AACACATCCA	240						
957	TGCCGCTCAC GTCAACATTG TCTGCCACCG CTGGACCCGG ATGGACATTG ACGGCAAGCC	300						
958		500						
959	ACACCCTCAC TCCTTCATCC GCGACAGCGA GGAGAAGCGG AATGTGCAGG TGGACGTGGT	360						
960 961		400						
962	CGAGGGCAAG GGCATCGATA TCAAGTCGTC TCTGTCCGGC CTGACCGTGC TGAAGAGCAC	420						
963	CAACTCGCAG TTCTGGGGCT TCCTGCGTGA CGAGTACACC ACACTTAAGG AGACCTGGGA	480						
964								
965 966	CCGTATCCTG AGCACCGACG TCGATGCCAC TTGGCAGTGG AAGAATTTCA GTGGACTCCA	540						
967	GGAGGTCCGC TCGCACGTGC CTAAGTTCGA TGCTACCTGG GCCACTGCTC GCGAGGTCAC	600						
968		000						
969	TCTGCCGACT TTTGCTGAAG ATAACAGTGC CAGCGTGCAG GCCACTATGT ACAAGATGGC	660						
970								
971 972	AGAGCAAATC CTGGCGCGCC AGCAGCTGAT CGAGACTGTC GAGTACTCGT TGCCTAACAA	720						
973	GCACTATTTC GAAATCGACC TGAGCTGGCA CAAGGGCCTC CAAAACACCG GCAAGAACGC	780						
974		,,,,						
975	CGAGGTCTTC GCTCCTCAGT CGGACCCCAA CGGTCTGATC AAGTGTACCG TCGGCCGGTC	840						
976 977	CTCTCTGAAG TCTAAATTGT AAACCAACAT GATTCTCACG TTCCGGAGTT TCCAAGGCAA	900						
978	CICICIONAG ICINATIGI AMACCANCAI GAIICICACG IICCGGAGII ICCAAGGCAA	900						
979	ACTGTATATA GTCTGGGATA GGGTATAGCA TTCATTCACT TGTTTTTTAC TTCCAAAAAA	960						
980								
981 982	АЛЛАЛАЛА АЛЛАЛАЛА АЛЛАЛАЛАЛ АЛЛАЛАЛАЛ АЛЛАЛАGGC CCG	1013						
983	(2) INFORMATION FOR SEQ ID NO:30:							
984								
985	(i) SEQUENCE CHARACTERISTICS:							
986	(A) LENGTH: 207 base pairs							
987 988	(B) TYPE: nucleic acid							
989	(C) STRANDEDNESS: single (D) TOPOLOGY: linear							
990	(-,							
991	(ii) MOLECULE TYPE: DNA (genomic)							
992 993	ALLEN TURATURE AND AND							
994	(iii) HYPOTHETICAL: NO							
995								
996	(vii) IMMEDIATE SOURCE:							
997	(B) CLONE: Synthetic GAL7 fragment							
998								
999 1000	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:							
1001	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:50:							
1002	CGCGTCTATA CTTCGGAGCA CTGTTGAGCG AAGGCTCATT AGATATATTT TCTGTCATTT	60						
1003								
1004	TCCTTAACCC AAAAATAAGG GAGAGGGTCC AAAAAGCGCT CGGACAACTG TTGACCGTGA	120						
1005 1006	TCCGAAGGAC TGGCTATACA GTGTTCACAA AATAGCCAAG CTGAAAATAA TGTGTAGCCT	180						
		TRO						

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1008	TTAGCTATGT TCAGTTAGTT TGGCATG					
1009						
1010	(2) INFORMATION FOR SEQ ID NO:31:					
1011	,					
1012	(i) SEQUENCE CHARACTERISTICS:					
1013	(A) LENGTH: 23 base pairs					
1014	(B) TYPE: nucleic acid					
1015	(C) STRANDEDNESS: single					
1016	(D) TOPOLOGY: linear					
1017						
1018	(ii) MOLECULE TYPE: DNA (genomic)					
1019						
1020	(iii) HYPOTHETICAL: NO					
1021						
1022	(vii) IMMEDIATE SOURCE:					
1023	(B) CLONE: Modified XbaI-MluI adapter					
1024						
1025	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:					
1026						
1027	CTAGGCTAGC GGGCCCGCAT GCA	23				
1028						
1029	(2) INFORMATION FOR SEQ ID NO:32:					
1030						
1031	(i) SEQUENCE CHARACTERISTICS:					
1032	(A) LENGTH: 422 base pairs					
1033	(B) TYPE: nucleic acid					
1034	(C) STRANDEDNESS: single					
1035	(D) TOPOLOGY: linear					
1036						
1037	(ii) MOLECULE TYPE: DNA (genomic)					
1038						
1039	(iii) HYPOTHETICAL: NO					
1040						
1041						
1042	(vii) IMMEDIATE SOURCE:					
1043	(B) CLONE: Plasmid pSE1 "site binding to HindIII"					
1044	fragment					
1045						
1046						
1047	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:					
1048						
1049	AGCTGGCTCG CATCTCTCT TCACGCGCCC GCCGCCCTAC CTGAGGCCGC CATCCACGCC	60				
1050						
1051	GGTGAGTCGC GTTCTGCCGC CTCCCGCCTG TGGTGCCTCC TGAACTGCGT CCGCCGTCTA	120				
1052						
1053	GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA	180				
1054						
1055	GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT	240				
1056						
1057	CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT	300				
1058						
1059	CTGGGACCCC TAGGAAGGGC TTGGGGGTCC TCGTGCCCAA GGCAGGGAAC ATAGTGGTCC	360				
1060						

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1061	CAGGAAGGGG AGCAGAGGCA TCAGGGTGTC CACTTTGTCT CCGCAGCTCC TGAGCCTGCA	420
1062		
1063	GA	422
1064		
1065	(2) INFORMATION FOR SEQ ID NO:33:	
1066		
1067	(i) SEQUENCE CHARACTERISTICS:	
1068	(A) LENGTH: 77 base pairs	
1069	(B) TYPE: nucleic acid	
1070	(C) STRANDEDNESS: single	
1071	(D) TOPOLOGY: linear	
1072		
1073	(ii) MOLECULE TYPE: DNA (genomic)	
1074	(iii) HYPOTHETICAL: NO	
1075		
1076		
1077	(vii) IMMEDIATE SOURCE:	
1078	(B) CLONE: Synthetic HindIII-"site binding to BamHI"	
1079	fragment	
1080		
1081		
1082	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:	
1083	·	
1084	AGCTTGTCGA CTAATACGAC TCACTATAGG GCGGCCGCGG GCCCCTGCAG GAATTCGGAT	60
1085		
1086	CCCCCGGGTG ACTGACT	77
1087		
1088	(2) INFORMATION FOR SEQ ID NO:34:	
1089	(i) SEQUENCE CHARACTERISTICS:	
1090	(A) LENGTH: 61 base pairs	
1091	(B) TYPE: nucleic acid	
1092	(C) STRANDEDNESS: single	
1093	(D) TOPOLOGY: linear	•
1094		
1095	(ii) MOLECULE TYPE: DNA (genomic)	
1096		
1097	(iii) HYPOTHETICAL: NO	
1098		
1099		
1100	(vii) IMMEDIATE SOURCE:	
1101	(B) CLONE: Synthetic HindIII-AccI fragment	
1102		
1103		
1104	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:	
1105		
1106	AGCTTGCCGC CACTATGTCC GCAGTAAAAG CAGCCCGCTA CGGCAAGGAC AATGTCCGCG	60
1107		
1108	T	61
1109	(A) TURBULATON TO A A A A A A A A A A A A A A A A A A	
1110	(2) INFORMATION FOR SEQ ID NO:35:	
1111		
1112	(i) SEQUENCE CHARACTERISTICS:	
1113	(A) LENGTH: 920 base pairs	

Raw Sequence Listing

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1114	(1	B) TYPE: nu	cleic acid				
1115	(C) STRANDEDNESS: single						
1116	(D) TOPOLOGY: linear						
1117	· ·	-,					
1118	(ii) MO	LECULE TYPE	: DNA (gend	omic)			
1119	(55)		(30				
1120	(iii) HV	POTHETICAL:	NO		•		
1121	(111) 111	. OILLI I CALL.	110				
1122							
1123	(wii) TM	MEDIATE SOU	IDCE •				
1124	` '		indIII-Snal	or functions			
1125	(.	b) CLORE: E	imaili-sna	or rragment			
1126							
1127	(mi) CE	OMENOE DEC	DIDETON. C	30 TD WO-25	_		
1127	(XI) SE	GOENCE DESC	RIPTION: SI	EQ ID NO:35	•		
1128	N.C.COTTC.C.C.C.C.	a. am. mamaa					
1129	AGCTTGCCGC	CACTATGTCC	GCAGTAAAAG	CAGCCCGCTA	CGGCAAGGAC	AATGTCCGCG	60
1130	mama aa a aa m		a.aa.aa				
	TCTACAAGGT	TCACAAGGAC	GAGAAGACCG	GTGTCCAGAC	GGTGTACGAG	ATGACCGTCT	120
1132							
1133	GTGTGCTTCT	GGAGGGTGAG	ATTGAGACCT	CTTACACCAA	GGCCGACAAC	AGCGTCATTG	180
1134							
1135	TCGCAACCGA	CTCCATTAAG	AACACCATTT	ACATCACCGC	CAAGCAGAAC	CCCGTTACTC	240
1136							
1137	CTCCCGAGCT	GTTCGGCTCC	ATCCTGGGCA	CACACTTCAT	TGAGAAGTAC	AACCACATCC	300
1138							
1139	ATGCCGCTCA	CGTCAACATT	GTCTGCCACC	GCTGGACCCG	GATGGACATT	GACGGCAAGC	360
1140							
1141	CACACCCTCA	CTCCTTCATC	CGCGACAGCG	AGGAGAAGCG	GAATGTGCAG	GTGGACGTGG	420
1142							
1143	TCGAGGGCAA	GGGCATCGAT	ATCAAGTCGT	CTCTGTCCGG	CCTGACCGTG	CTGAAGAGCA	480
1144							
1145	CCAACTCGCA (GTTCTGGGGC	TTCCTGCGTG	ACGAGTACAC	CACACTTAAG	GAGACCTGGG	540
1146							
1147	ACCGTATCCT (GAGCACCGAC	GTCGATGCCA	CTTGGCAGTG	GAAGAATTTC	AGTGGACTCC	600
1148							
1149	AGGAGGTCCG (CTCGCACGTG	CCTAAGTTCG	ATGCTACCTG	GGCCACTGCT	CGCGAGGTCA	660
1150							
1151	CTCTGAAGAC	ITTTGCTGAA	GATAACAGTG	CCAGCGTGCA	GGCCACTATG	TACAAGATGG	720
1152							
1153	CAGAGCAAAT (CCTGGCGCGC	CAGCAGCTGA	TCGAGACTGT	CGAGTACTCG	TTGCCTAACA	780
1154							
1155	AGCACTATTT (CGAAATCGAC	CTGAGCTGGC	ACAAGGGCCT	CCAAAACACC	GGCAAGAACG	840
1156							
1157	CCGAGGTCTT (CGCTCCTCAG	TCGGACCCCA	ACGGTCTGAT	CAAGTGTACC	GTCGGCCGGT	900
1158							
1159	CCTCTCTGAA	STCTAAATTG					920

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SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/07/659,408

DATE: 10/23/91 TIME: 11:14:19

LINE ERROR

ORIGINAL TEXT

38 Wrong application Serial Number
219 Response Exceeds Line Limitations
268 Response Exceeds Line Limitations
319 Response Exceeds Line Limitations
339 Response Exceeds Line Limitations
1044 Response Exceeds Line Limitations
1079 Response Exceeds Line Limitations
1079 Response Exceeds Line Limitations

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SEQUENCE MISSING ITEM REPORT PATENT APPLICATION US/07/659,408

DATE: 10/23/91 TIME: 11:14:19

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA APPLICATION NUMBER FILING DATE

PAGE: 1

LINE ORIGINAL TEXT

SEQUENCE CORRECTION REPORT PATENT APPLICATION US/07/659,408

CORRECTED TEXT

DATE: 10/23/91 TIME: 11:14:19